

SEQUENCE LISTING

(1) General Information

- (i) APPLICANT: SANTEN PHARMACEUTICAL CO., LTD.
- (ii) TITLE OF INVENTION: Novel Polypeptide Having Water Channel Activity and DNA sequence
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SANTEN PHARMACEUTICAL CO., LTD.
 - (B) STREET: 9 ? 19 Shimoshinjo 3-chome Higashiyodogawa-Ku
 - (C) CITY: Osaka
 - (D) STATE: Osaka
 - (E) COUNTRY: JAPAN
 - (F) ZIP: 533-0021
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB, storage
 - (B) COMPUTER: IBM PS/2 or compatibles
 - (C) OPERATING SYSTEM: WINDOWS 95/97
 - (D) SOFTWARE: Microsoft Word 97
- (vi) CURRENT APPLICATION DATE:
 - (A) APPLICATION NUMBER: 09/381,810
 - (B) FILING DATE: 19-OCT-1999
 - (C) CLASSIFICATION: 435
- (vii) PRIOR APPLICATION DATE
 - (A) APPLICATION NUMBER: JP09 094845
 - (B) FILING DATE: 28-MAR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Burton A. Amernick
 - (B) REGISTRATION NUMBER: 24852
 - (C) REFERENCE/DOCKET NUMBER: 1581/00156
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202)331-7111
 - (B) FAX: (202)293-6229

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH F342 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY F linear
- (ii) MORECULE TYPE F peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```

Met Val Gln Ala Ser Gly His Arg Arg Ser Thr Arg Gly Ser Lys Met
      5              10              15
Val Ser Trp Ser Val Ile Ala Lys Ile Gln Glu Ile Leu Gln Arg Lys
      20              25              30
Met Val Arg Glu Phe Leu Ala Glu Phe Met Ser Thr Tyr Val Met Met
      35              40              45
Val Phe Gly Leu Gly Ser Val Ala His Met Val Leu Asn Lys Lys Tyr
      50              55              60
Gly Ser Tyr Leu Gly Val Asn Leu Gly Phe Gly Phe Gly Val Thr Met
      65              70              75              80
Gly Val His Val Ala Gly Arg Ile Ser Gly Ala His Met Asn Ala Ala
      85              90              95
Val Thr Phe Ala Asn Cys Ala Leu Gly Arg Val Pro Trp Arg Lys Phe

```

09849980-050501

```

      100              105              110
Pro Val Tyr Val Leu Gly Gln Phe Leu Gly Ser Phe Leu Ala Ala Ala
      115              120              125
Thr Ile Tyr Ser Leu Phe Tyr Thr Ala Ile Leu His Phe Ser Gly Gly
      130              135              140
Gln Leu Met Val Thr Gly Pro Val Ala Thr Ala Gly Ile Phe Ala Thr
145              150              155              160
Tyr Leu Pro Asp His Met Thr Leu Trp Arg Gly Phe Leu Asn Glu Ala
      165              170              175
Trp Leu Thr Gly Met Leu Gln Leu Cys Leu Phe Ala Thr Thr Asp Gln
      180              185              190
Glu Asn Asn Pro Ala Leu Pro Gly Thr Glu Ala Leu Val Ile Gly Ile
      195              200              205
Leu Val Val Ile Ile Gly Val Ser Leu Gly Met Asn Thr Gly Tyr Ala
      210              215              220
Ile Asn Pro Ser Arg Asp Leu Pro Pro Arg Ile Phe Thr Phe Ile Ala
225              230              235              240
Gly Trp Gly Lys Gln Val Phe Ser Asn Gly Glu Asn Trp Trp Trp Val
      245              250              255
Pro Val Val Ala Pro Leu Leu Gly Ala Tyr Leu Gly Gly Ile Ile Tyr
      260              265              270
Leu Val Phe Ile Gly Ser Thr Ile Pro Arg Glu Pro Leu Lys Leu Glu
      275              280              285
Asp Ser Val Ala Tyr Glu Asp His Gly Ile Thr Val Leu Pro Lys Met
      290              295              300
Gly Ser His Glu Pro Thr Ile Ser Pro Leu Thr Pro Val Ser Val Ser
305              310              315              320
Pro Ala Asn Arg Ser Ser Val His Pro Ala Pro Pro Leu His Glu Ser
      325              330              335
Met Ala Leu Glu His Phe
      340

```

- (2) INFORMATION FOR SEQ ID No F2
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH F1258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY F linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens
 - (B) TISSUE TYPE: fat tissue
- (ix) FEATURE:
- (A) NAME/KEY: exon
 - (B) LOCATION F173..1198
 - (C) IDENTIFICATION METHOD: by experiment
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

GGCTCTGGAC TGGGGACACA GGGATAGCTG AGCCCCAGCT GGGGGTGGAA GCTGAGCCAG 60
GGACAGTCAC GGAGGAACAA GATCAAGATG CGCTGTAAC T GAGAAGCCCC CAAGGCGGAG 120
GCTGAGAATC AGAGACATTT CAGCAGACAT CTACAAATCT GAAAGACAAA AC ATG GTT 178
                                         Met Val
                                         1
CAA GCA TCC GGG CAC AGG CGG TCC ACC CGT GGC TCC AAA ATG GTC TCC 226
Gln Ala Ser Gly His Arg Arg Ser Thr Arg Gly Ser Lys Met Val Ser
      5              10              15

```

TGG	TCC	GTG	ATA	GCA	AAG	ATC	CAG	GAA	ATA	CTG	CAG	AGG	AAG	ATG	GTG		274
Trp	Ser	Val	Ile	Ala	Lys	Ile	Gln	Glu	Ile	Leu	Gln	Arg	Lys	Met	Val		
	20					25					30						
CGA	GAG	TTC	CTG	GCC	GAG	TTC	ATG	AGC	ACA	TAT	GTC	ATG	ATG	GTA	TTC		322
Arg	Glu	Phe	Leu	Ala	Glu	Phe	Met	Ser	Thr	Tyr	Val	Met	Met	Val	Phe		
	35				40					45					50		
GGC	CTT	GGT	TCC	GTG	GCC	CAT	ATG	GTT	CTA	AAT	AAA	AAA	TAT	GGG	AGC		370
Gly	Leu	Gly	Ser	Val	Ala	His	Met	Val	Leu	Asn	Lys	Lys	Tyr	Gly	Ser		
				55				60						65			
TAC	CTT	GGT	GTC	AAC	TTG	GGT	TTT	GGC	TTC	GGA	GTC	ACC	ATG	GGA	GTG		418
Tyr	Leu	Gly	Val	Asn	Leu	Gly	Phe	Gly	Phe	Gly	Val	Thr	Met	Gly	Val		
			70				75					80					
CAC	GTG	GCA	GGC	CGC	ATC	TCT	GGA	GCC	CAC	ATG	AAC	GCA	GCT	GTG	ACC		466
His	Val	Ala	Gly	Arg	Ile	Ser	Gly	Ala	His	Met	Asn	Ala	Ala	Val	Thr		
	85					90				95							
TTT	GCT	AAC	TGT	GCG	CTG	GGC	CGC	GTG	CCC	TGG	AGG	AAG	TTT	CCG	GTC		514
Phe	Ala	Asn	Cys	Ala	Leu	Gly	Arg	Val	Pro	Trp	Arg	Lys	Phe	Pro	Val		
	100				105					110							
TAT	GTG	CTG	GGG	CAG	TTC	CTG	GGC	TCC	TTC	CTG	GCG	GCT	GCC	ACC	ATC		562
Tyr	Val	Leu	Gly	Gln	Phe	Leu	Gly	Ser	Phe	Leu	Ala	Ala	Ala	Thr	Ile		
	115			120						125					130		
TAC	AGT	CTC	TTC	TAC	ACG	GCC	ATT	CTC	CAC	TTT	TCG	GGT	GGA	CAG	CTG		610
Tyr	Ser	Leu	Phe	Tyr	Thr	Ala	Ile	Leu	His	Phe	Ser	Gly	Gly	Gln	Leu		
			135						140					145			
ATG	GTG	ACC	GGT	CCC	GTC	GCT	ACA	GCT	GGC	ATT	TTT	GCC	ACC	TAC	CTT		658
Met	Val	Thr	Gly	Pro	Val	Ala	Thr	Ala	Gly	Ile	Phe	Ala	Thr	Tyr	Leu		
			150					155				160					
CCT	GAT	CAC	ATG	ACA	TTG	TGG	CGG	GGC	TTC	CTG	AAT	GAG	GCG	TGG	CTG		706
Pro	Asp	His	Met	Thr	Leu	Trp	Arg	Gly	Phe	Leu	Asn	Glu	Ala	Trp	Leu		
		165					170					175					
ACC	GGG	ATG	CTC	CAG	CTG	TGT	CTC	TTC	GCC	ATC	ACG	GAC	CAG	GAG	AAC		754
Thr	Gly	Met	Leu	Gln	Leu	Cys	Leu	Phe	Ala	Thr	Thr	Asp	Gln	Glu	Asn		
	180					185					190						
AAC	CCA	GCA	CTG	CCA	GGA	ACA	GAG	GCG	CTG	GTG	ATA	GGC	ATC	CTC	GTG		802
Asn	Pro	Ala	Leu	Pro	Gly	Thr	Glu	Ala	Leu	Val	Ile	Gly	Ile	Leu	Val		
	195			200						205					210		
GTC	ATC	ATC	GGG	GTG	TCC	CTT	GGC	ATG	AAC	ACA	GGA	TAT	GCC	ATC	AAC		850
Val	Ile	Ile	Gly	Val	Ser	Leu	Gly	Met	Asn	Thr	Gly	Tyr	Ala	Ile	Asn		
			215														

